



SEQUENCE LISTING

<110> DeBonte, Lorin R.
Fan, Zhegong
Miao, Guo-Hua

<120> FATTY ACID DESATURASES AND MUTANT SEQUENCES THEREOF

<130> 07148-063003

<140> US 09/771,904

<141> 2001-01-29

<150> US 08/874,109

<151> 1997-06-12

<160> 70

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1155

<212> DNA

<213> Brassica napus

<220>

<221> CDS

<222> (1)...(1152)

<223> Wild type Fad2

<221> misc_feature

<222> 205

<223> n = a, g, c, or t/u

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gaa acc gac acc atc aag cgc gta ccc tgc gag aca ccg ccc ttc act 96
Glu Thr Asp Thr Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr
20 25 30

gtc gga gaa ctc aag aaa gca atc cca ccg cac tgt ttc aaa cgc tcg 144
Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser
35 40 45

atc cct cgc tct ttc tcc tac ctc atc tgg gac atc atc ata gcc tcc 192
Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser
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tgc ttc tac tac ttc gcc acc act tac ttc cct ctc ctc cct cac cct 240
Cys Phe Tyr Tyr Xaa Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro

65	70	75	80	
ctc tcc tac ttc gcc tgg cct ctc tac tgg gcc tgc caa ggg tgc gtc				288
Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val	85	90	95	
cta acc ggc gtc tgg gtc ata gcc cac gaa tgc ggc cac cac gcc ttc				336
Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe	100	105	110	
agc gac tac cag tgg ctt gac gac acc gtc ggt ctc atc ttc cac tcc				384
Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser	115	120	125	
ttc ctc ctc gtc cct tac ttc tcc tgg aag tac agt cat cgc agc cac				432
Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Ser His	130	135	140	
cat tcc aac act ggc tcc ctc gag aga gac gaa gtg ttt gtc ccc aag				480
His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys	145	150	155	160
aag aag tca gac atc aag tgg tac ggc aag tac ctc aac aac cct ttg				528
Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu	165	170	175	
gga cgc acc gtg atg tta acg gtt cag ttc act ctc ggc tgg ccg ttg				576
Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu	180	185	190	
tac tta gcc ttc aac gtc tcg gga aga cct tac gac ggc ggc ttc cgt				624
Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Arg	195	200	205	
tgc cat ttc cac ccc aac gct ccc atc tac aac gac cgc gag cgt ctc				672
Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu	210	215	220	
cag ata tac atc tcc gac gct ggc atc ctc gcc gtc tgc tac ggt ctc				720
Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu	225	230	235	240
ttc cgt tac gcc gcc ggc cag gga gtg gcc tcg atg gtc tgc ttc tac				768
Phe Arg Tyr Ala Ala Gly Gln Gly Val Ala Ser Met Val Cys Phe Tyr	245	250	255	
gga gtc ccg ctt ctg att gtc aat ggt ttc ctc gtg ttg atc act tac				816
Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr	260	265	270	
ttg cag cac acg cat cct tcc ctg cct cac tac gat tcg tcc gag tgg				864
Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp	275	280	285	

gat tgg ttc agg gga gct ttg gct acc gtt gac aga gac tac gga atc 912
 Asp Trp Phe Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile
 290 295 300

ttg aac aag gtc ttc cac aat att acc gac acg cac gtg gcc cat cat 960
 Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His
 305 310 315 320

ccg ttc tcc acg atg ccg cat tat cac gcg atg gaa gct acc aag gcg 1008
 Pro Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala
 325 330 335

ata aag ccg ata ctg gga gag tat tat cag ttc gat ggg acg ccg gtg 1056
 Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val
 340 345 350

gtt aag gcg atg tgg agg gag gcg aag gag tgt atc tat gtg gaa ccg 1104
 Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro
 355 360 365

gac agg caa ggt gag aag aaa ggt gtg ttc tgg tac aac aat aag tta 1152
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tga 1155

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<211> 384

<212> PRT

<213> Brassica napus

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<223> Xaa = Phe, Leu, Ile, or Val

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 Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser
 35 40 45
 Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser
 50 55 60
 Cys Phe Tyr Tyr Xaa Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro
 65 70 75 80
 Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val
 85 90 95
 Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe
 100 105 110
 Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser
 115 120 125
 Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Ser His
 130 135 140

His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys
 145 150 155 160
 Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu
 165 170 175
 Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu
 180 185 190
 Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Arg
 195 200 205
 Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu
 210 215 220
 Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu
 225 230 235 240
 Phe Arg Tyr Ala Ala Gly Gln Gly Val Ala Ser Met Val Cys Phe Tyr
 245 250 255
 Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr
 260 265 270
 Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp
 275 280 285
 Asp Trp Phe Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile
 290 295 300
 Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His
 305 310 315 320
 Pro Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala
 325 330 335
 Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val
 340 345 350
 Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro
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<211> 1155

<212> DNA

<213> Brassica napus

<220>

<221> CDS

<222> (1)...(1152)

<223> G to A transversion mutation at nucleotide 316

<221> misc_feature

<222> 205

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gaa acc gac acc atc aag cgc gta ccc tgc gag aca ccg ccc ttc act
 Glu Thr Asp Thr Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr
 20 25 30

96

gtc gga gaa ctc aag aaa gca atc cca ccg cac tgt ttc aaa cgc tcg	144
Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser	
35 40 45	
atc cct cgc tct ttc tcc tac ctc atc tgg gac atc atc ata gcc tcc	192
Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser	
50 55 60	
tgc ttc tac tac ntc gcc acc act tac ttc cct ctc ctc cct cac cct	240
Cys Phe Tyr Tyr Xaa Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro	
65 70 75 80	
ctc tcc tac ttc gcc tgg cct ctc tac tgg gcc tgc caa ggg tgc gtc	288
Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val	
85 90 95	
cta acc ggc gtc tgg gtc ata gcc cac aag tgc ggc cac cac gcc ttc	336
Leu Thr Gly Val Trp Val Ile Ala His Lys Cys Gly His His Ala Phe	
100 105 110	
agc gac tac cag tgg ctt gac gac acc gtc ggt ctc atc ttc cac tcc	384
Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser	
115 120 125	
ttc ctc ctc gtc cct tac ttc tcc tgg aag tac agt cat cgc agc cac	432
Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Ser His	
130 135 140	
cat tcc aac act ggc tcc ctc gag aga gac gaa gtg ttt gtc ccc aag	480
His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys	
145 150 155 160	
aag aag tca gac atc aag tgg tac ggc aag tac ctc aac aac cct ttg	528
Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu	
165 170 175	
gga cgc acc gtg atg tta acg gtt cag ttc act ctc ggc tgg ccg ttg	576
Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu	
180 185 190	
tac tta gcc ttc aac gtc tcg gga aga cct tac gac ggc ggc ttc cgt	624
Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Arg	
195 200 205	
tgc cat ttc cac ccc aac gct ccc atc tac aac gac cgc gag cgt ctc	672
Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu	
210 215 220	
cag ata tac atc tcc gac gct ggc atc ctc gcc gtc tgc tac ggt ctc	720
Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu	
225 230 235 240	

ttc	cgt	tac	gcc	gcc	ggc	cag	gga	gtg	gcc	tcg	atg	gtc	tgc	ttc	tac	768
Phe	Arg	Tyr	Ala	Ala	Gly	Gln	Gly	Val	Ala	Ser	Met	Val	Cys	Phe	Tyr	
			245						250					255		

gga	gtc	ccg	ctt	ctg	att	gtc	aat	ggg	ttc	ctc	gtg	ttg	atc	act	tac	816
Gly	Val	Pro	Leu	Leu	Ile	Val	Asn	Gly	Phe	Leu	Val	Leu	Ile	Thr	Tyr	
			260					265					270			

ttg	cag	cac	acg	cat	cct	tcc	ctg	cct	cac	tac	gat	tcg	tcc	gag	tgg	864
Leu	Gln	His	Thr	His	Pro	Ser	Leu	Pro	His	Tyr	Asp	Ser	Ser	Glu	Trp	
			275					280					285			

gat	tgg	ttc	agg	gga	gct	ttg	gct	acc	gtt	gac	aga	gac	tac	gga	atc	912
Asp	Trp	Phe	Arg	Gly	Ala	Leu	Ala	Thr	Val	Asp	Arg	Asp	Tyr	Gly	Ile	
			290				295					300				

ttg	aac	aag	gtc	ttc	cac	aat	att	acc	gac	acg	cac	gtg	gcc	cat	cat	960
Leu	Asn	Lys	Val	Phe	His	Asn	Ile	Thr	Asp	Thr	His	Val	Ala	His	His	
			305			310					315				320	

ccg	ttc	tcc	acg	atg	ccg	cat	tat	cac	gcg	atg	gaa	gct	acc	aag	gcg	1008
Pro	Phe	Ser	Thr	Met	Pro	His	Tyr	His	Ala	Met	Glu	Ala	Thr	Lys	Ala	
				325					330					335		

ata	aag	ccg	ata	ctg	gga	gag	tat	tat	cag	ttc	gat	ggg	acg	ccg	gtg	1056
Ile	Lys	Pro	Ile	Leu	Gly	Glu	Tyr	Tyr	Gln	Phe	Asp	Gly	Thr	Pro	Val	
			340					345					350			

gtt	aag	gcg	atg	tgg	agg	gag	gcg	aag	gag	tgt	atc	tat	gtg	gaa	ccg	1104
Val	Lys	Ala	Met	Trp	Arg	Glu	Ala	Lys	Glu	Cys	Ile	Tyr	Val	Glu	Pro	
			355				360					365				

gac	agg	caa	ggg	gag	aag	aaa	ggg	gtg	ttc	tgg	tac	aac	aat	aag	tta	1152
Asp	Arg	Gln	Gly	Glu	Lys	Lys	Gly	Val	Phe	Trp	Tyr	Asn	Asn	Lys	Leu	
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tga																1155
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<210> 4

<211> 384

<212> PRT

<213> Brassica napus

<220>

<223> Xaa = Phe, Leu, Ile, or Val

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			20					25					30			
Val	Gly	Glu	Leu	Lys	Lys	Ala	Ile	Pro	Pro	His	Cys	Phe	Lys	Arg	Ser	
			35				40						45			

Ile	Pro	Arg	Ser	Phe	Ser	Tyr	Leu	Ile	Trp	Asp	Ile	Ile	Ile	Ala	Ser
	50					55					60				
Cys	Phe	Tyr	Tyr	Xaa	Ala	Thr	Thr	Tyr	Phe	Pro	Leu	Leu	Pro	His	Pro
65					70					75					80
Leu	Ser	Tyr	Phe	Ala	Trp	Pro	Leu	Tyr	Trp	Ala	Cys	Gln	Gly	Cys	Val
				85					90					95	
Leu	Thr	Gly	Val	Trp	Val	Ile	Ala	His	Lys	Cys	Gly	His	His	Ala	Phe
			100					105					110		
Ser	Asp	Tyr	Gln	Trp	Leu	Asp	Asp	Thr	Val	Gly	Leu	Ile	Phe	His	Ser
	115					120						125			
Phe	Leu	Leu	Val	Pro	Tyr	Phe	Ser	Trp	Lys	Tyr	Ser	His	Arg	Ser	His
130						135					140				
His	Ser	Asn	Thr	Gly	Ser	Leu	Glu	Arg	Asp	Glu	Val	Phe	Val	Pro	Lys
145					150					155					160
Lys	Lys	Ser	Asp	Ile	Lys	Trp	Tyr	Gly	Lys	Tyr	Leu	Asn	Asn	Pro	Leu
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Gly	Arg	Thr	Val	Met	Leu	Thr	Val	Gln	Phe	Thr	Leu	Gly	Trp	Pro	Leu
			180					185					190		
Tyr	Leu	Ala	Phe	Asn	Val	Ser	Gly	Arg	Pro	Tyr	Asp	Gly	Gly	Phe	Arg
	195					200						205			
Cys	His	Phe	His	Pro	Asn	Ala	Pro	Ile	Tyr	Asn	Asp	Arg	Glu	Arg	Leu
210						215					220				
Gln	Ile	Tyr	Ile	Ser	Asp	Ala	Gly	Ile	Leu	Ala	Val	Cys	Tyr	Gly	Leu
225					230					235					240
Phe	Arg	Tyr	Ala	Ala	Gly	Gln	Gly	Val	Ala	Ser	Met	Val	Cys	Phe	Tyr
				245					250					255	
Gly	Val	Pro	Leu	Leu	Ile	Val	Asn	Gly	Phe	Leu	Val	Leu	Ile	Thr	Tyr
			260					265					270		
Leu	Gln	His	Thr	His	Pro	Ser	Leu	Pro	His	Tyr	Asp	Ser	Ser	Glu	Trp
	275						280					285			
Asp	Trp	Phe	Arg	Gly	Ala	Leu	Ala	Thr	Val	Asp	Arg	Asp	Tyr	Gly	Ile
290						295					300				
Leu	Asn	Lys	Val	Phe	His	Asn	Ile	Thr	Asp	Thr	His	Val	Ala	His	His
305					310					315					320
Pro	Phe	Ser	Thr	Met	Pro	His	Tyr	His	Ala	Met	Glu	Ala	Thr	Lys	Ala
				325					330					335	
Ile	Lys	Pro	Ile	Leu	Gly	Glu	Tyr	Tyr	Gln	Phe	Asp	Gly	Thr	Pro	Val
			340					345					350		
Val	Lys	Ala	Met	Trp	Arg	Glu	Ala	Lys	Glu	Cys	Ile	Tyr	Val	Glu	Pro
	355						360					365			
Asp	Arg	Gln	Gly	Glu	Lys	Lys	Gly	Val	Phe	Trp	Tyr	Asn	Asn	Lys	Leu
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<211> 1155

<212> DNA

<213> Brassica napus

<220>

<221> CDS

<222> (1)...(1152)

<223> Wild type Fad2

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gaa acc gac aac atc aag cgc gta ccc tgc gag aca ccg ccc ttc act	96
Glu Thr Asp Asn Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr	
20 25 30	
gtc gga gaa ctc aag aaa gca atc cca ccg cac tgt ttc aaa cgc tcg	144
Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser	
35 40 45	
atc cct cgc tct ttc tcc tac ctc atc tgg gac atc atc ata gcc tcc	192
Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser	
50 55 60	
tgc ttc tac tac gtc gcc acc act tac ttc cct ctc ctc cct cac cct	240
Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro	
65 70 75 80	
ctc tcc tac ttc gcc tgg cct ctc tac tgg gcc tgc cag ggc tgc gtc	288
Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val	
85 90 95	
cta acc ggc gtc tgg gtc ata gcc cac gag tgc ggc cac cac gcc ttc	336
Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe	
100 105 110	
agc gac tac cag tgg ctg gac gac acc gtc ggc ctc atc ttc cac tcc	384
Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser	
115 120 125	
ttc ctc ctc gtc cct tac ttc tcc tgg aag tac agt cat cga cgc cac	432
Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His	
130 135 140	
cat tcc aac act ggc tcc ctc gag aga gac gaa gtg ttt gtc ccc aag	480
His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys	
145 150 155 160	
aag aag tca gac atc aag tgg tac ggc aag tac ctc aac aac cct ttg	528
Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu	
165 170 175	
gga cgc acc gtg atg tta acg gtt cag ttc act ctc ggc tgg cct ttg	576
Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu	
180 185 190	
tac tta gcc ttc aac gtc tcg ggg aga cct tac gac ggc ggc ttc gct	624
Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Ala	
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tgc cat ttc cac ccc aac gct ccc atc tac aac gac cgc gag cgt ctc	672
Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu	
210 215 220	
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Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu	
225 230 235 240	
tac cgc tac gct gct gtc caa gga gtt gcc tcg atg gtc tgc ttc tac	768
Tyr Arg Tyr Ala Ala Val Gln Gly Val Ala Ser Met Val Cys Phe Tyr	
245 250 255	
gga gtt ccg ctt ctg att gtc aat ggg ttc tta gtt ttg atc act tac	816
Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr	
260 265 270	
ttg cag cac acg cat cct tcc ctg cct cac tat gac tcg tct gag tgg	864
Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp	
275 280 285	
gat tgg ttg agg gga gct ttg gcc acc gtt gac aga gac tac gga atc	912
Asp Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile	
290 295 300	
ttg aac aag gtc ttc cac aat atc acg gac acg cac gtg gcg cat cac	960
Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His	
305 310 315 320	
ctg ttc tcg acc atg ccg cat tat cat gcg atg gaa gct acg aag gcg	1008
Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala	
325 330 335	
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Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Leu His Gly Thr Pro Val	
340 345 350	
gtt aag gcg atg tgg agg gag gcg aag gag tgt atc tat gtg gaa ccg	1104
Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro	
355 360 365	
gac agg caa ggt gag aag aaa ggt gtg ttc tgg tac aac aat aag tta	1152
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<211> 384	
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Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser						
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Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ala Ser						
	50			55		60
Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro						
65		70			75	80
Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val						
	85			90		95
Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe						
	100			105		110
Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser						
	115			120		125
Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His						
	130			135		140
His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys						
145		150			155	160
Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu						
	165			170		175
Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu						
	180			185		190
Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Ala						
	195			200		205
Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu						
	210			215		220
Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu						
225		230			235	240
Tyr Arg Tyr Ala Ala Val Gln Gly Val Ala Ser Met Val Cys Phe Tyr						
	245			250		255
Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr						
	260			265		270
Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp						
	275			280		285
Asp Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile						
	290			295		300
Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His						
305		310			315	320
Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala						
	325			330		335
Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Leu His Gly Thr Pro Val						
	340			345		350
Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro						
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Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu						
370		375			380	

<210> 7

<211> 1155

<212> DNA

<213> Brassica napus

<220>

<221> CDS

<222> (1)...(1152)

<223> T to A transversion mutation at nucleotide 515

<400> 7

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Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser	
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gaa acc gac aac atc aag cgc gta ccc tgc gag aca ccg ccc ttc act	96
Glu Thr Asp Asn Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr	
20 25 30	
gtc gga gaa ctc aag aaa gca atc cca ccg cac tgt ttc aaa cgc tcg	144
Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser	
35 40 45	
atc cct cgc tct ttc tcc tac ctc atc tgg gac atc atc ata gcc tcc	192
Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser	
50 55 60	
tgc ttc tac tac gtc gcc acc act tac ttc cct ctc ctc cct cac cct	240
Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro	
65 70 75 80	
ctc tcc tac ttc gcc tgg cct ctc tac tgg gcc tgc cag ggc tgc gtc	288
Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val	
85 90 95	
cta acc ggc gtc tgg gtc ata gcc cac gag tgc ggc cac cac gcc ttc	336
Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe	
100 105 110	
agc gac tac cag tgg ctg gac gac acc gtc ggc ctc atc ttc cac tcc	384
Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser	
115 120 125	
ttc ctc ctc gtc cct tac ttc tcc tgg aag tac agt cat cga cgc cac	432
Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His	
130 135 140	
cat tcc aac act ggc tcc ctc gag aga gac gaa gtg ttt gtc ccc aag	480
His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys	
145 150 155 160	
aag aag tca gac atc aag tgg tac ggc aag tac cac aac aac cct ttg	528
Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr His Asn Asn Pro Leu	
165 170 175	
gga cgc acc gtg atg tta acg gtt cag ttc act ctc ggc tgg cct ttg	576
Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu	
180 185 190	

tac tta gcc ttc aac gtc tcg ggg aga cct tac gac ggc ggc ttc gct Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Ala 195 200 205	624
tgc cat ttc cac ccc aac gct ccc atc tac aac gac cgc gag cgt ctc Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu 210 215 220	672
cag ata tac atc tcc gac gct ggc atc ctc gcc gtc tgc tac ggt ctc Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu 225 230 235 240	720
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ttg cag cac acg cat cct tcc ctg cct cac tat gac tcg tct gag tgg Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp 275 280 285	864
gat tgg ttg agg gga gct ttg gcc acc gtt gac aga gac tac gga atc Asp Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile 290 295 300	912
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ctg ttc tcg acc atg ccg cat tat cat gcg atg gaa gct acg aag gcg Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala 325 330 335	1008
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gac agg caa ggt gag aag aaa ggt gtg ttc tgg tac aac aat aag tta Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu 370 375 380	1152
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<213> Brassica napus

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 35 40 45
 Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ala Ser
 50 55 60
 Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro
 65 70 75 80
 Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val
 85 90 95
 Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe
 100 105 110
 Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser
 115 120 125
 Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His
 130 135 140
 His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys
 145 150 155 160
 Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr His Asn Asn Pro Leu
 165 170 175
 Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu
 180 185 190
 Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Ala
 195 200 205
 Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu
 210 215 220
 Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu
 225 230 235 240
 Tyr Arg Tyr Ala Ala Val Gln Gly Val Ala Ser Met Val Cys Phe Tyr
 245 250 255
 Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr
 260 265 270
 Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp
 275 280 285
 Asp Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile
 290 295 300
 Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His
 305 310 315 320
 Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala
 325 330 335
 Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Leu His Gly Thr Pro Val
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<212> DNA

<213> Brassica napus

<220>

<221> CDS

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gaa	acc	gac	aac	atc	aag	cgc	gta	ccc	tgc	gag	aca	ccg	ccc	ttc	act	96
Glu	Thr	Asp	Asn	Ile	Lys	Arg	Val	Pro	Cys	Glu	Thr	Pro	Pro	Phe	Thr	
			20					25					30			

gtc	gga	gaa	ctc	aag	aaa	gca	atc	cca	ccg	cac	tgt	ttc	aaa	cgc	tcg	144
Val	Gly	Glu	Leu	Lys	Lys	Ala	Ile	Pro	Pro	His	Cys	Phe	Lys	Arg	Ser	
		35					40					45				

atc	cct	cgc	tct	ttc	tcc	tac	ctc	atc	tgg	gac	atc	atc	ata	gcc	tcc	192
Ile	Pro	Arg	Ser	Phe	Ser	Tyr	Leu	Ile	Trp	Asp	Ile	Ile	Ile	Ala	Ser	
	50						55				60					

tgc	ttc	tac	tac	gtc	gcc	acc	act	tac	ttc	cct	ctc	ctc	cct	cac	cct	240
Cys	Phe	Tyr	Tyr	Val	Ala	Thr	Thr	Tyr	Phe	Pro	Leu	Leu	Pro	His	Pro	
65					70					75					80	

ctc	tcc	tac	ttc	gcc	tgg	cct	ctc	tac	tgg	gcc	tgc	cag	ggc	tgc	gtc	288
Leu	Ser	Tyr	Phe	Ala	Trp	Pro	Leu	Tyr	Trp	Ala	Cys	Gln	Gly	Cys	Val	
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cta	acc	ggc	gtc	tgg	gtc	ata	gcc	cac	gag	tgc	ggc	cac	cac	gcc	ttc	336
Leu	Thr	Gly	Val	Trp	Val	Ile	Ala	His	Glu	Cys	Gly	His	His	Ala	Phe	
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agc	gac	tac	cag	tgg	ctg	gac	gac	acc	gtc	ggc	ctc	atc	ttc	cac	tcc	384
Ser	Asp	Tyr	Gln	Trp	Leu	Asp	Asp	Thr	Val	Gly	Leu	Ile	Phe	His	Ser	
		115					120					125				

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Phe	Leu	Leu	Val	Pro	Tyr	Phe	Ser	Trp	Lys	Tyr	Ser	His	Arg	Arg	His	
	130						135				140					

cat	tcc	aac	act	ggc	tcc	ctc	gag	aga	gac	gaa	gtg	ttt	gtc	ccc	aag	480
His	Ser	Asn	Thr	Gly	Ser	Leu	Glu	Arg	Asp	Glu	Val	Phe	Val	Pro	Lys	
145					150					155					160	

aag	aag	tca	gac	atc	aag	tgg	tac	ggc	aag	tac	ctc	aac	aac	cct	ttg	528
Lys	Lys	Ser	Asp	Ile	Lys	Trp	Tyr	Gly	Lys	Tyr	Leu	Asn	Asn	Pro	Leu	
				165					170					175		

gga cgc acc gtg atg tta acg gtt cag ttc act ctc ggc tgg cct ttg	576
Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu	
180 185 190	
tac tta gcc ttc aac gtc tcg ggg aga cct tac gac ggc ggc ttc gct	624
Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Ala	
195 200 205	
tgc cat ttc cac ccc aac gct ccc atc tac aac gac cgt gag cgt ctc	672
Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu	
210 215 220	
cag ata tac atc tcc gac gct ggc atc ctc gcc gtc tgc tac ggt ctc	720
Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu	
225 230 235 240	
tac cgc tac gct gct gtc caa gga gtt gcc tcg atg gtc tgc ttc tac	768
Tyr Arg Tyr Ala Val Gln Gly Val Ala Ser Met Val Cys Phe Tyr	
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Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr	
260 265 270	
ttg cag cac acg cat cct tcc ctg cct cac tat gac tcg tct gag tgg	864
Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp	
275 280 285	
gat tgg ttg agg gga gct ttg gcc acc gtt gac aga gac tac gga atc	912
Asp Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile	
290 295 300	
ttg aac aag gtc ttc cac aat atc acg gac acg cac gtg gcg cat cac	960
Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His	
305 310 315 320	
ctg ttc tcg acc atg ccg cat tat cat gcg atg gaa gct acg aag gcg	1008
Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala	
325 330 335	
ata aag ccg ata ctg gga gag tat tat cag ttc gat ggg acg ccg gtg	1056
Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val	
340 345 350	
gtt aag gcg atg tgg agg gag gcg aag gag tgt atc tat gtg gaa ccg	1104
Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro	
355 360 365	
gac agg caa ggt gag aag aaa ggt gtg ttc tgg tac aac aat aag tta	1152
Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu	
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			20					25					30		
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	50					55					60				
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Leu	Ser	Tyr	Phe	Ala	Trp	Pro	Leu	Tyr	Trp	Ala	Cys	Gln	Gly	Cys	Val
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Lys	Lys	Ser	Asp	Ile	Lys	Trp	Tyr	Gly	Lys	Tyr	Leu	Asn	Asn	Pro	Leu
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Gly	Arg	Thr	Val	Met	Leu	Thr	Val	Gln	Phe	Thr	Leu	Gly	Trp	Pro	Leu
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Tyr	Leu	Ala	Phe	Asn	Val	Ser	Gly	Arg	Pro	Tyr	Asp	Gly	Gly	Phe	Ala
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Cys	His	Phe	His	Pro	Asn	Ala	Pro	Ile	Tyr	Asn	Asp	Arg	Glu	Arg	Leu
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Gln	Ile	Tyr	Ile	Ser	Asp	Ala	Gly	Ile	Leu	Ala	Val	Cys	Tyr	Gly	Leu
225					230					235					240
Tyr	Arg	Tyr	Ala	Ala	Val	Gln	Gly	Val	Ala	Ser	Met	Val	Cys	Phe	Tyr
			245					250						255	
Gly	Val	Pro	Leu	Leu	Ile	Val	Asn	Gly	Phe	Leu	Val	Leu	Ile	Thr	Tyr
		260					265						270		
Leu	Gln	His	Thr	His	Pro	Ser	Leu	Pro	His	Tyr	Asp	Ser	Ser	Glu	Trp
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Asp	Trp	Leu	Arg	Gly	Ala	Leu	Ala	Thr	Val	Asp	Arg	Asp	Tyr	Gly	Ile
	290					295					300				
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Leu	Phe	Ser	Thr	Met	Pro	His	Tyr	His	Ala	Met	Glu	Ala	Thr	Lys	Ala
			325					330						335	
Ile	Lys	Pro	Ile	Leu	Gly	Glu	Tyr	Tyr	Gln	Phe	Asp	Gly	Thr	Pro	Val
		340					345						350		
Val	Lys	Ala	Met	Trp	Arg	Glu	Ala	Lys	Glu	Cys	Ile	Tyr	Val	Glu	Pro
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 <222> (1)...(1152)

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Glu Thr Asp Asn Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr	
20 25 30	
gtc gga gaa ctc aag aaa gca atc cca ccg cac tgt ttc aaa cgc tcg	144
Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser	
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atc cct cgc tct ttc tcc tac ctc atc tgg gac atc atc ata gcc tcc	192
Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser	
50 55 60	
tgc ttc tac tac gtc gcc acc act tac ttc cct ctc ctc cct cac cct	240
Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro	
65 70 75 80	
ctc tcc tac ttc gcc tgg cct ctc tac tgg gcc tgc cag ggc tgc gtc	288
Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val	
85 90 95	
cta acc ggc gtc tgg gtc ata gcc cac aag tgc ggc cac cac gcc ttc	336
Leu Thr Gly Val Trp Val Ile Ala His Lys Cys Gly His His Ala Phe	
100 105 110	
agc gac tac cag tgg ctg gac gac acc gtc ggc ctc atc ttc cac tcc	384
Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser	
115 120 125	
ttc ctc ctc gtc cct tac ttc tcc tgg aag tac agt cat cga cgc cac	432
Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His	
130 135 140	
cat tcc aac act ggc tcc ctc gag aga gac gaa gtg ttt gtc ccc aag	480
His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys	
145 150 155 160	

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Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu	
165 170 175	
gga cgc acc gtg atg tta acg gtt cag ttc act ctc ggc tgg cct ttg	576
Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu	
180 185 190	
tac tta gcc ttc aac gtc tcg ggg aga cct tac gac ggc ggc ttc gct	624
Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Ala	
195 200 205	
tgc cat ttc cac ccc aac gct ccc atc tac aac gac cgt gag cgt ctc	672
Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu	
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Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu	
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Tyr Arg Tyr Ala Val Gln Gly Val Ala Ser Met Val Cys Phe Tyr	
245 250 255	
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Gly Val Pro Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr	
260 265 270	
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Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp	
275 280 285	
gat tgg ttg agg gga gct ttg gcc acc gtt gac aga gac tac gga atc	912
Asp Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile	
290 295 300	
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Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His	
305 310 315 320	
ctg ttc tcg acc atg ccg cat tat cat gcg atg gaa gct acg aag gcg	1008
Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala	
325 330 335	
ata aag ccg ata ctg gga gag tat tat cag ttc gat ggg acg ccg gtg	1056
Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val	
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gtt aag gcg atg tgg agg gag gcg aag gag tgt atc tat gtg gaa ccg	1104
Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro	
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gac agg caa ggt gag aag aaa ggt gtg ttc tgg tac aac aat aag tta 1152
 Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu
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tga 1155

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<211> 384

<212> PRT

<213> Brassica napus

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 Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser
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 Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro
 65 70 75 80
 Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val
 85 90 95
 Leu Thr Gly Val Trp Val Ile Ala His Lys Cys Gly His His Ala Phe
 100 105 110
 Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser
 115 120 125
 Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His
 130 135 140
 His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys
 145 150 155 160
 Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu
 165 170 175
 Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu
 180 185 190
 Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Ala
 195 200 205
 Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu
 210 215 220
 Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu
 225 230 235 240
 Tyr Arg Tyr Ala Ala Val Gln Gly Val Ala Ser Met Val Cys Phe Tyr
 245 250 255
 Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr
 260 265 270
 Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp
 275 280 285
 Asp Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile
 290 295 300
 Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His
 305 310 315 320
 Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala

				325						330					335				
Ile	Lys	Pro	Ile	Leu	Gly	Glu	Tyr	Tyr	Gln	Phe	Asp	Gly	Thr	Pro	Val				
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Val	Lys	Ala	Met	Trp	Arg	Glu	Ala	Lys	Glu	Cys	Ile	Tyr	Val	Glu	Pro				
		355					360					365							
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gaa acc gac acc atc aag cgc gta ccc tgc gag aca ccg ccc ttc act	96
Glu Thr Asp Thr Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr	
20 25 30	
gtc gga gaa ctc aag aaa gca atc cca ccg cac tgt ttc aaa cgc tcg	144
Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser	
35 40 45	
atc cct cgc tct ttc tcc tac ctc atc tgg gac atc atc ata gcc tcc	192
Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser	
50 55 60	
tgc ttc tac tac gtc gcc acc act tac ttc cct ctc ctc cct cac cct	240
Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro	
65 70 75 80	
ctc tcc tac ttc gcc tgg cct ctc tac tgg gcc tgc caa ggg tgc gtc	288
Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val	
85 90 95	
cta acc ggc gtc tgg gtc ata gcc cac gag tgc ggc cac cac gcc ttc	336
Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe	
100 105 110	
agc gac tac cag tgg ctt gac gac acc gtc ggt ctc atc ttc cac tcc	384
Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser	
115 120 125	
ttc ctc ctc gtc cct tac ttc tcc tgg aag tac agt cat cga cgc cac	432
Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His	
130 135 140	

cat tcc aac act ggc tcc ctc gag aga gac gaa gtg ttt gtc ccc aag	480
His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys	
145 150 155 160	
aag aag tca gac atc aag tgg tac ggc aag tac ctc aac aac cct ttg	528
Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu	
165 170 175	
gga cgc acc gtg atg tta acg gtt cag ttc act ctc ggc tgg ccg ttg	576
Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu	
180 185 190	
tac tta gcc ttc aac gtc tcg gga aga cct tac gac ggc ggc ttc gct	624
Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Ala	
195 200 205	
tgc cat ttc cac ccc aac gct ccc atc tac aac gac cgc gag cgt ctc	672
Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu	
210 215 220	
cag ata tac atc tcc gac gct ggc atc ctc gcc gtc tgc tac ggt ctc	720
Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu	
225 230 235 240	
ttc cgt tac gcc gcc gcg cag gga gtg gcc tcg atg gtc tgc ttc tac	768
Phe Arg Tyr Ala Ala Ala Gln Gly Val Ala Ser Met Val Cys Phe Tyr	
245 250 255	
gga gtc ccg ctt ctg att gtc aat ggt ttc ctc gtg ttg atc act tac	816
Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr	
260 265 270	
ttg cag cac acg cat cct tcc ctg cct cac tac gat tcg tcc gag tgg	864
Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp	
275 280 285	
gat tgg ttg agg gga gct ttg gct acc gtt gac aga gac tac gga atc	912
Asp Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile	
290 295 300	
ttg aac aag gtc ttc cac aat att acc gac acg cac gtg gcg cat cat	960
Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His	
305 310 315 320	
ctg ttc tcc acg atg ccg cat tat cac gcg atg gaa gct acc aag gcg	1008
Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala	
325 330 335	
ata aag ccg ata ctg gga gag tat tat cag ttc gat ggg acg ccg gtg	1056
Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val	
340 345 350	

gtt aag gcg atg tgg agg gag gcg aag gag tgt atc tat gtg gaa ccg 1104
 Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro
 355 360 365

gac agg caa ggt gag aag aaa ggt gtg ttc tgg tac aac aat aag tta 1152
 Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu
 370 375 380

tga 1155

<210> 14

<211> 384

<212> PRT

<213> Brassica napus

<400> 14

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 Glu Thr Asp Thr Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr
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 Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser
 35 40 45
 Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser
 50 55 60
 Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro
 65 70 75 80
 Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val
 85 90 95
 Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe
 100 105 110
 Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser
 115 120 125
 Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His
 130 135 140
 His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys
 145 150 155 160
 Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu
 165 170 175
 Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu
 180 185 190
 Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Ala
 195 200 205
 Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu
 210 215 220
 Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu
 225 230 235 240
 Phe Arg Tyr Ala Ala Ala Gln Gly Val Ala Ser Met Val Cys Phe Tyr
 245 250 255
 Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr
 260 265 270
 Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp
 275 280 285
 Asp Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile

290	295	300
Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His		
305	310	315
Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala		
	325	330
Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val		
	340	345
Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro		
	355	360
Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu		
370	375	380

<210> 15

<211> 1155

<212> DNA

<213> Brassica napus

<220>

<221> CDS

<222> (1)...(1152)

<400> 15

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gaa acc gac acc atc aag cgc gta ccc tgc gag aca ccg ccc ttc act	96
Glu Thr Asp Thr Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr	
20 25 30	

gtc gga gaa ctc aag aaa gca atc cca ccg cac tgt ttc aaa cgc tcg	144
Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser	
35 40 45	

atc cct cgc tct ttc tcc tac ctc atc tgg gac atc atc ata gcc tcc	192
Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser	
50 55 60	

tgc ttc tac tac gtc gcc acc act tac ttc cct ctc ctc cct cac cct	240
Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro	
65 70 75 80	

ctc tcc tac ttc gcc tgg cct ctc tac tgg gcc tgc caa ggg tgc gtc	288
Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val	
85 90 95	

cta acc ggc gtc tgg gtc ata gcc cac gag tgc ggc cac cac gcc ttc	336
Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe	
100 105 110	

agc gac tac cag tgg ctt gac gac acc gtc ggt ctc atc ttc cac tcc	384
Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser	
115 120 125	

ttc ctc ctc gtc cct tac ttc tcc tgg aag tac agt cat cga cgc cac	432
Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His	
130 135 140	
cat tcc aac act ggc tcc ctc gag aga gac gaa gtg ttt gtc ccc aag	480
His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys	
145 150 155 160	
aag aag tca gac atc aag tgg tac ggc aag tac cac aac aac cct ttg	528
Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr His Asn Asn Pro Leu	
165 170 175	
gga cgc acc gtg atg tta acg gtt cag ttc act ctc ggc tgg ccg ttg	576
Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu	
180 185 190	
tac tta gcc ttc aac gtc tcg gga aga cct tac gac ggc ggc ttc gct	624
Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Ala	
195 200 205	
tgc cat ttc cac ccc aac gct ccc atc tac aac gac cgc gag cgt ctc	672
Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu	
210 215 220	
cag ata tac atc tcc gac gct ggc atc ctc gcc gtc tgc tac ggt ctc	720
Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu	
225 230 235 240	
ttc cgt tac gcc gcc gcg cag gga gtg gcc tcg atg gtc tgc ttc tac	768
Phe Arg Tyr Ala Ala Ala Gln Gly Val Ala Ser Met Val Cys Phe Tyr	
245 250 255	
gga gtc ccg ctt ctg att gtc aat ggt ttc ctc gtg ttg atc act tac	816
Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr	
260 265 270	
ttg cag cac acg cat cct tcc ctg cct cac tac gat tcg tcc gag tgg	864
Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp	
275 280 285	
gat tgg ttg agg gga gct ttg gct acc gtt gac aga gac tac gga atc	912
Asp Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile	
290 295 300	
ttg aac aag gtc ttc cac aat att acc gac acg cac gtg gcg cat cat	960
Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His	
305 310 315 320	
ctg ttc tcc acg atg ccg cat tat cac gcg atg gaa gct acc aag gcg	1008
Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala	
325 330 335	

ata aag ccg ata ctg gga gag tat tat cag ttc gat ggg acg ccg gtg 1056
 Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val
 340 345 350

gtt aag gcg atg tgg agg gag gcg aag gag tgt atc tat gtg gaa ccg 1104
 Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro
 355 360 365

gac agg caa ggt gag aag aaa ggt gtg ttc tgg tac aac aat aag tta 1152
 Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu
 370 375 380

tga 1155

<210> 16

<211> 384

<212> PRT

<213> Brassica napus

<400> 16

Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser
 1 5 10 15
 Glu Thr Asp Thr Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr
 20 25 30
 Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser
 35 40 45
 Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser
 50 55 60
 Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro
 65 70 75 80
 Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val
 85 90 95
 Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe
 100 105 110
 Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser
 115 120 125
 Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His
 130 135 140
 His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys
 145 150 155 160
 Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr His Asn Asn Pro Leu
 165 170 175
 Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu
 180 185 190
 Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Ala
 195 200 205
 Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu
 210 215 220
 Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu
 225 230 235 240
 Phe Arg Tyr Ala Ala Ala Gln Gly Val Ala Ser Met Val Cys Phe Tyr
 245 250 255
 Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr

			260					265					270				
Leu	Gln	His	Thr	His	Pro	Ser	Leu	Pro	His	Tyr	Asp	Ser	Ser	Glu	Trp		
		275					280					285					
Asp	Trp	Leu	Arg	Gly	Ala	Leu	Ala	Thr	Val	Asp	Arg	Asp	Tyr	Gly	Ile		
	290					295					300						
Leu	Asn	Lys	Val	Phe	His	Asn	Ile	Thr	Asp	Thr	His	Val	Ala	His	His		
305					310				315						320		
Leu	Phe	Ser	Thr	Met	Pro	His	Tyr	His	Ala	Met	Glu	Ala	Thr	Lys	Ala		
				325					330					335			
Ile	Lys	Pro	Ile	Leu	Gly	Glu	Tyr	Tyr	Gln	Phe	Asp	Gly	Thr	Pro	Val		
			340				345						350				
Val	Lys	Ala	Met	Trp	Arg	Glu	Ala	Lys	Glu	Cys	Ile	Tyr	Val	Glu	Pro		
	355					360					365						
Asp	Arg	Gln	Gly	Glu	Lys	Lys	Gly	Val	Phe	Trp	Tyr	Asn	Asn	Lys	Leu		
	370					375					380						

<210> 17

<211> 1155

<212> DNA

<213> Brassica napus

<220>

<221> CDS

<222> (1) ... (1152)

<400> 17

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Met	Gly	Ala	Gly	Gly	Arg	Met	Gln	Val	Ser	Pro	Pro	Ser	Lys	Lys	Ser		
1				5					10					15			

gaa	acc	gac	acc	atc	aag	cgc	gta	ccc	tgc	gag	aca	ccg	ccc	ttc	act		96
Glu	Thr	Asp	Thr	Ile	Lys	Arg	Val	Pro	Cys	Glu	Thr	Pro	Pro	Phe	Thr		
			20					25					30				

gtc	gga	gaa	ctc	aag	aaa	gca	atc	cca	ccg	cac	tgt	ttc	aaa	cgc	tcg		144
Val	Gly	Glu	Leu	Lys	Lys	Ala	Ile	Pro	Pro	His	Cys	Phe	Lys	Arg	Ser		
		35				40						45					

atc	cct	cgc	tct	ttc	tcc	tac	ctc	atc	tgg	gac	atc	atc	ata	gcc	tcc		192
Ile	Pro	Arg	Ser	Phe	Ser	Tyr	Leu	Ile	Trp	Asp	Ile	Ile	Ile	Ala	Ser		
	50					55					60						

tgc	ttc	tac	tac	gtc	gcc	acc	act	tac	ttc	cct	ctc	ctc	cct	cac	cct		240
Cys	Phe	Tyr	Tyr	Val	Ala	Thr	Thr	Tyr	Phe	Pro	Leu	Leu	Pro	His	Pro		
	65				70				75					80			

ctc	tcc	tac	ttc	gcc	tgg	cct	ctc	tac	tgg	gcc	tgc	caa	ggg	tgc	gtc		288
Leu	Ser	Tyr	Phe	Ala	Trp	Pro	Leu	Tyr	Trp	Ala	Cys	Gln	Gly	Cys	Val		
				85				90						95			

cta	acc	ggc	gtc	tgg	gtc	ata	gcc	cac	gag	tgc	ggc	cac	cac	gcc	ttc		336
Leu	Thr	Gly	Val	Trp	Val	Ile	Ala	His	Glu	Cys	Gly	His	His	Ala	Phe		
			100				105							110			

agc gac tac cag tgg ctt gac gac acc gtc ggt ctc atc ttc cac tcc Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser 115 120 125	384
ttc ctc ctc gtc cct tac ttc tcc tgg aag tac agt cat cga cgc cac Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His 130 135 140	432
cat tcc aac act ggc tcc ctc gag aga gac gaa gtg ttt gtc ccc aag His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys 145 150 155 160	480
aag aag tca gac atc aag tgg tac ggc aag tac ctc aac aac cct ttg Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu 165 170 175	528
gga cgc acc gtg atg tta acg gtt cag ttc act ctc ggc tgg ccg ttg Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu 180 185 190	576
tac tta gcc ttc aac gtc tcg gga aga cct tac gac ggc ggc ttc gct Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Ala 195 200 205	624
tgc cat ttc cac ccc aac gct ccc atc tac aac gac cgc gag cgt ctc Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu 210 215 220	672
cag ata tac atc tcc gac gct ggc atc ctc gcc gtc tgc tac ggt ctc Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu 225 230 235 240	720
ttc cgt tac gcc gcc gcg cag gga gtg gcc tcg atg gtc tgc ttc tac Phe Arg Tyr Ala Ala Ala Gln Gly Val Ala Ser Met Val Cys Phe Tyr 245 250 255	768
gga gtc ccg ctt ctg att gtc aat ggt ttc ctc gtg ttg atc act tac Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr 260 265 270	816
ttg cag cac acg cat cct tcc ctg cct cac tac gat tcg tcc gag tgg Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp 275 280 285	864
gat tgg ttg agg gga gct ttg gct acc gtt gac aga gac tac gaa atc Asp Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Glu Ile 290 295 300	912
ttg aac aag gtc ttc cac aat att acc gac acg cac gtg gcg cat cat Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His 305 310 315 320	960

ctg ttc tcc acg atg ccg cat tat cac gcg atg gaa gct acc aag gcg	1008
Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala	
325 330 335	

ata aag ccg ata ctg gga gag tat tat cag ttc gat ggg acg ccg gtg	1056
Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val	
340 345 350	

gtt aag gcg atg tgg agg gag gcg aag gag tgt atc tat gtg gaa ccg	1104
Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro	
355 360 365	

gac agg caa ggt gag aag aaa ggt gtg ttc tgg tac aac aat aag tta	1152
Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu	
370 375 380	

tga	1155
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<211> 384

<212> PRT

<213> Brassica napus

<400> 18

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Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser	
35 40 45	
Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser	
50 55 60	
Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro	
65 70 75 80	
Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val	
85 90 95	
Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe	
100 105 110	
Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser	
115 120 125	
Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His	
130 135 140	
His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys	
145 150 155 160	
Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu	
165 170 175	
Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu	
180 185 190	
Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Ala	
195 200 205	
Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu	
210 215 220	
Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu	

225		230		235		240									
Phe	Arg	Tyr	Ala	Ala	Ala	Gln	Gly	Val	Ala	Ser	Met	Val	Cys	Phe	Tyr
			245						250					255	
Gly	Val	Pro	Leu	Leu	Ile	Val	Asn	Gly	Phe	Leu	Val	Leu	Ile	Thr	Tyr
			260						265					270	
Leu	Gln	His	Thr	His	Pro	Ser	Leu	Pro	His	Tyr	Asp	Ser	Ser	Glu	Trp
		275							280				285		
Asp	Trp	Leu	Arg	Gly	Ala	Leu	Ala	Thr	Val	Asp	Arg	Asp	Tyr	Glu	Ile
	290						295				300				
Leu	Asn	Lys	Val	Phe	His	Asn	Ile	Thr	Asp	Thr	His	Val	Ala	His	His
305					310					315				320	
Leu	Phe	Ser	Thr	Met	Pro	His	Tyr	His	Ala	Met	Glu	Ala	Thr	Lys	Ala
				325					330					335	
Ile	Lys	Pro	Ile	Leu	Gly	Glu	Tyr	Tyr	Gln	Phe	Asp	Gly	Thr	Pro	Val
			340						345				350		
Val	Lys	Ala	Met	Trp	Arg	Glu	Ala	Lys	Glu	Cys	Ile	Tyr	Val	Glu	Pro
	355						360					365			
Asp	Arg	Gln	Gly	Glu	Lys	Lys	Gly	Val	Phe	Trp	Tyr	Asn	Asn	Lys	Leu
370						375					380				

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<220>
 <223> primer

<400> 19
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21

<210> 20
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 20
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21

<210> 21
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 <212> DNA
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<220>
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<400> 21
 gttatgaagc aaagaagaaa c

21

<210> 22

<211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 22
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<210> 23
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 <212> DNA
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<220>
 <223> primer

<400> 23
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<210> 24
 <211> 33
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<220>
 <223> primer

<400> 24
 cuacuacuac uatcatagaa gagaaagggtt cag 33

<210> 25
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 25
 caucauac aukatgggtg cacgtggaag aa 32

<210> 26
 <211> 33
 <212> DNA
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<220>
 <223> primer

<400> 26
 cuacuacuac uatctttcac catcatcata tcc 33

<210> 27
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 <213> *Arabidopsis thaliana*

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 Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser Phe
 20 25 30

<210> 28
 <211> 30
 <212> PRT
 <213> *Glycine max*

<400> 28
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 Gln Trp Val Asp Asp Val Val Gly Leu Thr Leu His Ser Thr
 20 25 30

<210> 29
 <211> 30
 <212> PRT
 <213> *Zea mays*

<400> 29
 Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe Ser Asp Tyr
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 Ser Leu Leu Asp Asp Val Val Gly Leu Val Leu His Ser Ser
 20 25 30

<210> 30
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 <212> PRT
 <213> *Ricinus communis*

<400> 30
 Trp Val Met Ala His Asp Cys Gly His His Ala Phe Ser Asp Tyr Gln
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 Leu Leu Asp Asp Val Val Gly Leu Ile Leu His Ser Cys
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<210> 31
 <211> 29
 <212> PRT
 <213> *Arabidopsis thaliana*

<400> 31
 Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His His
 1 5 10 15
 Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val

20

25

<210> 32
 <211> 29
 <212> PRT
 <213> Glycine max

<400> 32
 Leu Leu Val Pro Tyr Phe Ser Trp Lys Ile Ser His Arg Arg His His
 1 5 10 15
 Ser Asn Thr Gly Ser Leu Asp Arg Asp Glu Val Phe Val
 20 25

<210> 33
 <211> 29
 <212> PRT
 <213> Zea mays

<400> 33
 Leu Met Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His His
 1 5 10 15
 Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val
 20 25

<210> 34
 <211> 29
 <212> PRT
 <213> Ricinus communis

<400> 34
 Leu Leu Val Pro Tyr Phe Ser Trp Lys His Ser His Arg Arg His His
 1 5 10 15
 Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val
 20 25

<210> 35
 <211> 36
 <212> PRT
 <213> Arabidopsis thaliana

<400> 35
 Asp Arg Asp Tyr Gly Ile Leu Asn Lys Val Phe His Asn Ile Thr Asp
 1 5 10 15
 Thr His Val Ala His His Leu Phe Ser Thr Met Pro His Tyr Asn Ala
 20 25 30
 Met Glu Ala Thr
 35

<210> 36
 <211> 36
 <212> PRT
 <213> Glycine max

<400> 36

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Asp Arg Asp Tyr Gly Ile Leu Asn Lys Val Phe His His Ile Thr Asp
 1           5           10           15
Thr His Val Ala His His Leu Phe Ser Thr Met Pro His Tyr His Ala
           20           25           30
Met Glu Ala Thr
           35

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<210> 37

<211> 36

<212> PRT

<213> Zea mays

<400> 37

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Asp Arg Asp Tyr Gly Ile Leu Asn Arg Val Phe His Asn Ile Thr Asp
 1           5           10           15
Thr His Val Ala His His Leu Phe Ser Thr Met Pro His Tyr His Ala
           20           25           30
Met Glu Ala Thr
           35

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<210> 38

<211> 27

<212> PRT

<213> Ricinus communis

<400> 38

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Asp Arg Asp Tyr Gly Ile Leu Asn Lys Val Phe His Asn Ile Thr Asp
 1           5           10           15
Thr Gln Val Ala His His Leu Phe Thr Met Pro
           20           25

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<210> 39

<211> 16

<212> PRT

<213> Arabidopsis thaliana

<400> 39

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Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu Gly Arg Ile Met
 1           5           10           15

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<210> 40

<211> 16

<212> PRT

<213> Glycine max

<400> 40

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Val Ala Trp Phe Ser Leu Tyr Leu Asn Asn Pro Leu Gly Arg Ala Val
 1           5           10           15

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<210> 41

<211> 16

<212> PRT

<213> Zea mays

<400> 41

Pro Trp Tyr Thr Pro Tyr Val Tyr Asn Asn Pro Val Gly Arg Val Val
1 5 10 15

<210> 42

<211> 16

<212> PRT

<213> Ricinus communis

<400> 42

Ile Arg Trp Tyr Ser Lys Tyr Leu Asn Asn Pro Pro Gly Arg Ile Met
1 5 10 15

<210> 43

<211> 22

<212> PRT

<213> Arabidopsis thaliana

<400> 43

Trp Ala Leu Phe Val Leu Gly His Asp Cys Gly His Gly Ser Phe Ser
1 5 10 15
Asn Asp Pro Lys Leu Asn
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<210> 44

<211> 22

<212> PRT

<213> Brassica napus

<400> 44

Trp Ala Leu Phe Val Leu Gly His Asp Cys Gly His Gly Ser Phe Ser
1 5 10 15
Asn Asp Pro Arg Leu Asn
20

<210> 45

<211> 22

<212> PRT

<213> Glycine max

<400> 45

Trp Ala Leu Phe Val Leu Gly His Asp Cys Gly His Gly Ser Phe Ser
1 5 10 15
Asn Asn Ser Lys Leu Asn
20

<210> 46

<211> 22

<212> PRT

<213> Arabidopsis thaliana

<400> 46

Trp Ala Ile Phe Val Leu Gly His Asp Cys Gly His Gly Ser Phe Ser
 1 5 10 15
 Asp Ile Pro Leu Leu Asn
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<210> 47

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> exemplary motif

<400> 47

Asp Arg Asp Tyr Gly Ile Leu Asn Lys Val
 1 5 10

<210> 48

<211> 22

<212> PRT

<213> Glycine max

<400> 48

Trp Ala Leu Phe Val Leu Gly His Asp Cys Gly His Gly Ser Phe Ser
 1 5 10 15
 Asp Ser Pro Pro Leu Asn
 20

<210> 49

<211> 29

<212> PRT

<213> Arabidopsis thaliana

<400> 49

Ile Leu Val Pro Tyr His Gly Trp Arg Ile Ser His Arg Thr His His
 1 5 10 15
 Gln Asn His Gly His Val Glu Asn Asp Glu Ser Trp His
 20 25

<210> 50

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> exemplary motif

<400> 50

Asp Arg Asp Tyr Glu Ile Leu Asn Lys Val
 1 5 10

<210> 51

<211> 29
 <212> PRT
 <213> Glycine max

<400> 51
 Ile Leu Val Pro Tyr His Gly Trp Arg Ile Ser His Arg Thr His His
 1 5 10 15
 Gln His His Gly His Ala Glu Asn Asp Glu Ser Trp His
 20 25

<210> 52
 <211> 29
 <212> PRT
 <213> Arabidopsis thaliana

<400> 52
 Ile Leu Val Pro Tyr His Gly Trp Arg Ile Ser His Arg Thr His His
 1 5 10 15
 Gln Asn His Gly His Val Glu Asn Asp Glu Ser Trp Val
 20 25

<210> 53
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> exemplary motif

<400> 53
 Lys Tyr His Asn Asn Pro
 1 5

<210> 54
 <211> 29
 <212> PRT
 <213> Glycine max

<400> 54
 Ile Leu Val Pro Tyr His Gly Trp Arg Ile Ser His Arg Thr His His
 1 5 10 15
 Gln Asn His Gly His Ile Glu Lys Asp Glu Ser Trp Val
 20 25

<210> 55
 <211> 6
 <212> PRT
 <213> Brassica napus

<400> 55
 Gly His Asp Cys Ala His
 1 5

<210> 56

<211> 6
 <212> PRT
 <213> Brassica napus

<400> 56
 Gly His Lys Cys Gly His
 1 5

<210> 57
 <211> 6
 <212> PRT
 <213> Brassica napus

<220>
 <221> VARIANT
 <223> amino acid residues 94-99 of Canola-Fad3

<400> 57
 Gly His Asp Cys Gly His
 1 5

<210> 58
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> exemplary motif

<400> 58
 His Lys Cys Gly His
 1 5

<210> 59
 <211> 12
 <212> DNA
 <213> Phaseolus vulgaris

<400> 59.
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12

<210> 60
 <211> 5
 <212> PRT
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<220>
 <223> exemplary motif

<400> 60
 His Glu Cys Gly His
 1 5

<210> 61

<211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> exemplary motif

<400> 61
 His Arg Arg His His
 1 5

<210> 62
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> exemplary motif

<400> 62
 His Arg Thr His His
 1 5

<210> 63
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> exemplary motif

<400> 63
 His Val Ala His His
 1 5

<210> 64
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> exemplary motif

<400> 64
 Lys Tyr Leu Asn Asn Pro
 1 5

<210> 65
 <211> 29
 <212> PRT
 <213> Brassica napus

<400> 65
 Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe Ser Asp Tyr

1	5	10	15
Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser			
20	25		

<210> 66
 <211> 36
 <212> PRT
 <213> Brassica napus

<400> 66
Asp Arg Asp Tyr Gly Ile Leu Asn Lys Val Phe His Asn Ile Thr Asp
1 5 10 15
Thr His Val Ala His His Leu Phe Ser Thr Met Pro His Tyr His Ala
20 25 30
Met Glu Ala Thr
35

<210> 67
 <211> 16
 <212> PRT
 <213> Brassica napus

<400> 67
Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu Gly Arg Thr Val
1 5 10 15

<210> 68
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> exemplary motif

<400> 68
Ala His Lys Cys Gly His
1 5

<210> 69
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> exemplary motif

<400> 69
Ala His Glu Cys Gly His
1 5

<210> 70
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> exemplary motif

<400> 70
His Asp Cys Gly His
1 5